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=> d his

     (FILE 'HOME' ENTERED AT 07:32:49 ON 12 NOV 2003)

     INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS,
     DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, ...' ENTERED AT 07:33:37 ON 12 NOV
     2003
               SEA NUCLEOTIDE-SUGAR EPIMERASE
               ---------
               1   FILE AGRICOLA
               2   FILE AQUASCI
               7   FILE BIOSIS
               5   FILE BIOTECHNO
               4   FILE CABA
               1   FILE CANCERLIT
               9   FILE CAPLUS
               1   FILE DISSABS
               5   FILE EMBASE
               6   FILE ESBIOBASE
               1   FILE FSTA
             222   FILE GENBANK
               4   FILE LIFESCI
               6   FILE MEDLINE
               2   FILE PASCAL
               6   FILE SCISEARCH
               4   FILE TOXCENTER
              12   FILE USPATFULL
L1              QUE NUCLEOTIDE-SUGAR EPIMERASE
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     FILE 'USPATFULL, CAPLUS, BIOSIS, ESBIOBASE, MEDLINE, SCISEARCH,
     BIOTECHNO, EMBASE, CABA, LIFESCI, TOXCENTER, AQUASCI, PASCAL, AGRICOLA,
     CANCERLIT' ENTERED AT 07:35:19 ON 12 NOV 2003
L2              1 S L1 AND (SIALIC ACID OR NANA OR NEURAMINIC ACID)
L3              0 S N-ACETYLGLUCOSAMINE EPIMERASE-2
L4             34 S N-ACETYLGLUCOSAMINE EPIMERASE
L5             22 DUP REM L4 (12 DUPLICATES REMOVED)
L6              6 S L5 AND (SIALIC ACID OR NANA OR NEURAMINIC ACID)

     FILE 'REGISTRY' ENTERED AT 07:42:50 ON 12 NOV 2003
                E UDP-N-ACETYLGLUCOSAMINE-2-EPIMERASE/CN
L7              1 S E4
                E N-ACETYLGLUCOSAMINE-2-EPIMERASE/CN
```

L6 ANSWER 4 OF 6 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2003:36800542 BIOTECHNO
TITLE: GlcNAc 2-epimerase can serve a catabolic role in **sialic acid** metabolism
AUTHOR: Luchansky S.J.; Yarema K.J.; Takahashi S.; Bertozzi C.R.
CORPORATE SOURCE: C.R. Bertozzi, Department of Chemistry, University of California, Berkeley, CA 94720, United States. E-mail: bertozzi@cchem.berkeley.edu
SOURCE: Journal of Biological Chemistry, (07 MAR 2003), 278/10 (8035-8042), 48 reference(s)
CODEN: JBCHA3 ISSN: 0021-9258
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English

AB **Sialic acid** is a major determinant of carbohydrate-receptor interactions in many systems pertinent to human health and disease. N-Acetylmannosamine (ManNAc) is the first committed intermediate in the **sialic acid** biosynthetic pathway; thus, the mechanisms that control intracellular ManNAc levels are important regulators of **sialic acid** production. UDP-GlcNAc 2-epimerase and GlcNAc 2-epimerase are two enzymes capable of generating ManNAc from UDP-GlcNAc and GlcNAc, respectively. Whereas the former enzyme has been shown to direct metabolic flux toward **sialic acid** in vivo, the function of the latter enzyme is unclear. Here we study the effects of GlcNAc 2-epimerase expression on **sialic acid** production in cells. A key tool we developed for this study is a cell-permeable, small molecule inhibitor of GlcNAc 2-epimerase designed based on mechanistic principles. Our results indicate that, unlike UDP-GlcNAc 2-epimerase, which promotes biosynthesis of **sialic acid**, GlcNAc 2-epimerase can serve a catabolic role, diverting metabolic flux away from the **sialic acid** pathway.

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=> d l2 ibib ab

L2   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER:        2001:634533  CAPLUS
DOCUMENT NUMBER:         136:242629
TITLE:                   The complete sequence of the 1,683-Kb pSymB
                         megaplasmid from the N2-fixing endosymbiont
                         Sinorhizobium meliloti
AUTHOR(S):               Finan, Turlough M.; Weidner, Stefan; Wong, Kim;
                         Buhrmester, Jens; Chain, Patrick; Vorholter, Frank J.;
                         Hernandez-Lucas, Ismael; Becker, Anke; Cowie, Alison;
                         Gouzy, Jerome; Golding, Brian; Puhler, Alfred
CORPORATE SOURCE:        Department of Biology, McMaster University, Hamilton,
                         ON, L8S 4K1, Can.
SOURCE:                  Proceedings of the National Academy of Sciences of the
                         United States of America (2001), 98(17), 9889-9894
                         CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER:               National Academy of Sciences
DOCUMENT TYPE:           Journal
LANGUAGE:                English
AB   Anal. of the 1683,333-nt sequence of the pSymB megaplasmid from the
     symbiotic N2-fixing bacterium Sinorhizobium meliloti revealed that the
     replicon has a high gene d. with a total of 1570 protein-coding regions,
     with few insertion elements and regions duplicated elsewhere in the
     genome.  The only copies of an essential arg-tRNA gene and the minCDE
     genes are located on pSymB.  Almost 20% of the pSymB sequence carries
     genes encoding solute uptake systems, most of which were of the
     ATP-binding cassette family.  Many previously unsuspected genes involved
     in polysaccharide biosynthesis were identified and these, together with
     the two known distinct exopolysaccharide synthesis gene clusters, show
     that 14% of the pSymB sequence is dedicated to polysaccharide synthesis.
     Other recognizable gene clusters include many involved in catabolic
     activities such as protocatechuate utilization and phosphonate degrdn.
     The functions of these genes are consistent with the notion that pSymB
     plays a major role in the saprophytic competence of the bacteria in the
     soil environment.
REFERENCE COUNT:         76    THERE ARE 76 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT


=> s N-acetylglucosamine epimerase-2
  13 FILES SEARCHED...
L3            0 N-ACETYLGLUCOSAMINE EPIMERASE-2

=> s N-acetylglucosamine epimerase
L4           34 N-ACETYLGLUCOSAMINE EPIMERASE

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5           22 DUP REM L4 (12 DUPLICATES REMOVED)

=> s l5 and (sialic acid or NANA or neuraminic acid)
   6 FILES SEARCHED...
  11 FILES SEARCHED...
L6            6 L5 AND (SIALIC ACID OR NANA OR NEURAMINIC ACID)

=> d l6 ibib ab 1-6

L6   ANSWER 1 OF 6  USPATFULL on STN
ACCESSION NUMBER:        2003:60089  USPATFULL
TITLE:                   Nucleotide sequence of the Haemophilus influenzae Rd
                         genome, fragments thereof, and uses thereof
INVENTOR(S):             Fleischmann, Robert D., Gaithersburg, MD, United States
```

Adams, Mark D., N. Potomac, MD, United States
White, Owen, Gaithersburg, MD, United States
Smith, Hamilton O., Towson, MD, United States
Venter, J. Craig, Potomac, MD, United States

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6528289	B1	20030304
APPLICATION INFO.:	US 2000-643990		20000823 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1995-487429, filed on 7 Jun 1995 Continuation-in-part of Ser. No. US 1995-426787, filed on 21 Apr 1995, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Martinell, James
LEGAL REPRESENTATIVE: Human Genome Sciences, Inc.
NUMBER OF CLAIMS: 23
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 47 Drawing Figure(s); 47 Drawing Page(s)
LINE COUNT: 4428
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the sequencing of the entire genome of Haemophilus influenzae Rd, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies over 1700 protein encoding fragments of the genome and identifies, by position relative to a unique Not I restriction endonuclease site, any regulatory elements which modulate the expression of the protein encoding fragments of the Haemophilus genome.

L6 ANSWER 2 OF 6 USPATFULL on STN
ACCESSION NUMBER: 94:66407 USPATFULL
TITLE: Process for the production of activated **sialic acids**

INVENTOR(S): Kittelmann, Matthias, Kartauserstrasse 88, 7800 Freiburg, Germany, Federal Republic of
Ghisalba, Oreste, Eschenweg 3, 4153 Reinach, Switzerland
Klein, Teresa, Mariengartenstrasse 6, 5170 Julich, Germany, Federal Republic of
Kragl, Udo, 665 Takarazuka-Shi, Takatsukasa-3-6-32 Nigawa, Greenheight 105, Japan
Wandrey, Christian, Wolfshovener Strasse 139, 5170 Julich, Germany, Federal Republic of

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5334514		19940802
APPLICATION INFO.:	US 1993-152269		19931112 (8)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1992-915474, filed on 16 Jul 1992, now abandoned

	NUMBER	DATE
PRIORITY INFORMATION:	CH 1991-2119	19910717

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Lilling, Herbert J.
LEGAL REPRESENTATIVE: Kaiser, Karen G., Fishman, Irving M.

NUMBER OF CLAIMS: 15
EXEMPLARY CLAIM: 1
LINE COUNT: 1301
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to a process for the production of cytidine 5'-monophosphosialic acids which comprises reacting a **sialic acid** with cytidine 5'-triphosphate in the presence of a cell extract of a naturally occurring microorganism having cytidine 5'-monophospho-N-acetylneuraminic acid synthetase activity, the extract optionally having been subjected to one purification step.

L6 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2001:49966 BIOSIS
DOCUMENT NUMBER: PREV200100049966
TITLE: The structure of UDP-N-acetylglucosamine 2-epimerase reveals homology to phosphoglycosyl transferases.
AUTHOR(S): Campbell, Robert E.; Mosimann, Steven C.; Tanner, Martin E. [Reprint author]; Strynadka, Natalie C. J.
CORPORATE SOURCE: Department of Chemistry, University of British Columbia, Vancouver, British Columbia, V6T 1Z1, Canada mtanner@chem.ubc.ca; natalie@byron.biochem.ubc.ca
SOURCE: Biochemistry, (December 12, 2000) Vol. 39, No. 49, pp. 14993-15001. print.
CODEN: BICHAW. ISSN: 0006-2960.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 24 Jan 2001
Last Updated on STN: 12 Feb 2002
AB Bacterial UDP-N-acetylglucosamine 2-epimerase catalyze the reversible epimerization at C-2 of UDP-N-acetylglucosamine (UDP-GlcNAc) and thereby provides bacteria with UDP-N-acetylmannosamine (UDP-ManNAc), the activated donor of ManNAc residues. ManNAc is critical for several processes in bacteria, including formation of the antiphagocytic capsular polysaccharide of pathogens such as Streptococcus pneumoniae types 19F and 19A. We have determined the X-ray structure (2.5 ANG) of UDP-GlcNAc 2-epimerase with bound UDP and identified a previously unsuspected structural homology with the enzymes glycogen phosphorylase and T4 phage beta-glucosyltransferase. The relationship to these phosphoglycosyl transferases is very intriguing in terms of possible similarities in the catalytic mechanisms. Specifically, this observation is consistent with the proposal that the UDP-GlcNAc 2-epimerase-catalyzed elimination and re-addition of UDP to the glycal intermediate may proceed through a transition state with significant oxocarbenium ion-like character. The homodimeric epimerase is composed of two similar alpha/beta/alpha sandwich domains with the active site located in the deep cleft at the domain interface. Comparison of the multiple copies in the asymmetric unit has revealed that the epimerase can undergo a 10degree interdomain rotation that is implicated in the regulatory mechanism. A structure-based sequence alignment has identified several basic residues in the active site that may be involved in the proton transfer at C-2 or stabilization of the proposed oxocarbenium ion-like transition state. This insight into the structure of the bacterial epimerase is applicable to the homologous N-terminal domain of the bifunctional mammalian UDP-GlcNAc "hydrolyzing" 2-epimerase/ManNAc kinase that catalyzes the rate-determining step in the **sialic acid** biosynthetic pathway.

L6 ANSWER 4 OF 6 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
ACCESSION NUMBER: 2003:36800542 BIOTECHNO
TITLE: GlcNAc 2-epimerase can serve a catabolic role in **sialic acid** metabolism
AUTHOR: Luchansky S.J.; Yarema K.J.; Takahashi S.; Bertozzi C.R.
CORPORATE SOURCE: C.R. Bertozzi, Department of Chemistry, University of California, Berkeley, CA 94720, United States.

E-mail: bertozzi@cchem.berkeley.edu
SOURCE: Journal of Biological Chemistry, (07 MAR 2003), 278/10 (8035-8042), 48 reference(s)
CODEN: JBCHA3 ISSN: 0021-9258
DOCUMENT TYPE: Journal; Article
COUNTRY: United States
LANGUAGE: English
SUMMARY LANGUAGE: English
AB **Sialic acid** is a major determinant of carbohydrate-receptor interactions in many systems pertinent to human health and disease. N-Acetylmannosamine (ManNAc) is the first committed intermediate in the **sialic acid** biosynthetic pathway; thus, the mechanisms that control intracellular ManNAc levels are important regulators of **sialic acid** production. UDP-GlcNAc 2-epimerase and GlcNAc 2-epimerase are two enzymes capable of generating ManNAc from UDP-GlcNAc and GlcNAc, respectively. Whereas the former enzyme has been shown to direct metabolic flux toward **sialic acid** in vivo, the function of the latter enzyme is unclear. Here we study the effects of GlcNAc 2-epimerase expression on **sialic acid** production in cells. A key tool we developed for this study is a cell-permeable, small molecule inhibitor of GlcNAc 2-epimerase designed based on mechanistic principles. Our results indicate that, unlike UDP-GlcNAc 2-epimerase, which promotes biosynthesis of **sialic acid**, GlcNAc 2-epimerase can serve a catabolic role, diverting metabolic flux away from the **sialic acid** pathway.

L6 ANSWER 5 OF 6 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
ACCESSION NUMBER: 1985:15127922 BIOTECHNO
TITLE: The metabolism of **sialic acids** in isolated rat colonic mucosal cells
AUTHOR: Corfield A.P.; Clamp J.R.; Wagner S.A.
CORPORATE SOURCE: University of Bristol Department of Medicine Laboratories, Bristol Royal Infirmary, Bristol BS2 8HW, United Kingdom.
SOURCE: Biochemical Journal, (1985), 226/1 (163-174)
CODEN: BIJOAK
DOCUMENT TYPE: Journal; Article
COUNTRY: United Kingdom
LANGUAGE: English
AB The activities of ten enzymes involved in **sialic acid** metabolism were measured in colonic mucosal cells from rats and compared with those in liver. A methodology was devised that enabled all ten enzyme activities to be evaluated in a single rat colon preparation. Enzyme assays with radioactively labelled substrates were developed for maximum sensitivity, and the identification of substrates and products was carefully checked to assess the contribution of contaminants to enzyme reactions with low activity. The activities of most enzymes involved in the biosynthesis of N-acetyl-D-**neuraminic acid** (NeuAc) from UDP-N-acetyl-D-glucosamine were found to be more than 20-fold lower than those in liver. The activities of CMP-NeuAc synthase, N-acetyl-D-glucosamine 2-epimerase, N-acetyl-D-glucosamine kinase, sialyltransferase and sialidase were similar to or 2-4-fold lower than in liver. The biosynthesis of NeuAc via its 9-phosphate was demonstrated in the 100,000 g supernatant of colonic-cell homogenates by enzymic assay and precursor experiments with N-acetyl.cents..sup.1.sup.4C!-mannosamine. No alternative route for NeuAc formation could be detected. The 100,000 g supernatant fractions of liver, kidney and colonic mucosal cells utilized N-acetyl.cents..sup.1.sup.4C!mannosamine with differing efficiencies. Radioactive products identified as **sialic acid** biosynthetic intermediates amounted to 49%, 0.04% and 5.6% of added precursor in liver, kidney and colon respectively. Catabolism of labelled precursor to non-hexosamine products was high in kidney and colonic

mucosal-cell fractions.

L6 ANSWER 6 OF 6 PASCAL COPYRIGHT 2003 INIST-CNRS. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 1993-0286066 PASCAL
TITLE (IN ENGLISH): Clinical and biochemical studies in an American child with sialuria
AUTHOR: KRASNEWICH D. M.; TIETZE F.; KRAUSE W.; PRETZLAFF R.; WENGER D. A.; DIWADKAR V.; GAHL W. A.
CORPORATE SOURCE: NIH, national inst. child health human development, human genetics branch, Bethesda MD 20892, United States
SOURCE: Biochemical medicine and metabolic biology, (1993), 49(1), 90-96, 18 refs.
ISSN: 0885-4505 CODEN: BMMBES
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United States
LANGUAGE: English
AVAILABILITY: INIST-14095, 354000038486530100

=> file reg

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	59.04	60.90

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-0.65	-0.65

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DICTIONARY FILE UPDATES: 11 NOV 2003 HIGHEST RN 615535-77-8

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> e UDP-N-acetylglucosamine-2-epimerase/CN

E1	1	UDP-N-ACETYLGLUCOSAMINE-1-CARBOXYVINYLTRANSFERASE (MYCOBACTERIUM LEPRAE STRAIN TN GENE MURA)/CN
E2	1	UDP-N-ACETYLGLUCOSAMINE-1-PHOSPHATE TRANSFERASE (PROCHLOROCOCCUS MARINUS PASTORIS STRAIN MED4 GENE PMM1227)/CN
E3	0 -->	UDP-N-ACETYLGLUCOSAMINE-2-EPIMERASE/CN
E4	1	UDP-N-ACETYLGLUCOSAMINE-2-EPIMERASE / N-ACETYLMANNOSAMINE KINASE (HUMAN GENE UDP-GLCNAC-2-EPIMERASE)/CN
E5	1	UDP-N-ACETYLGLUCOSAMINE-2-EPIMERASE NEUC (LEPTOSPIRA INTERROGANS ICTEROHAEMORRHAGIAE STRAIN 56601 GENE NNAC)/CN

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E6            1     UDP-N-ACETYLGLUCOSAMINE-4-EPIMERASE/CN
E7            1     UDP-N-ACETYLGLUCOSAMINE-6-PHOSPHOGALACTOSE SULFATE/CN
E8            1     UDP-N-ACETYLGLUCOSAMINE-DOLICHOL PHOSPHATE N-ACETYLGLUCOSAMI
                    NYLTRANSFERASE/CN
E9            1     UDP-N-ACETYLGLUCOSAMINE-DOLICHYL PHOSPHATE N-ACETYLGLUCOSAMI
                    NE PHOSPHOTRANSFERASE (SULFOLOBUS ACIDOCALDARIUS ORF2)/CN
E10           1     UDP-N-ACETYLGLUCOSAMINE-DOLICHYL PHOSPHATE N-ACETYLGLUCOSAMI
                    NE PHOSPHOTRANSFERASE (SULFOLOBUS TOKODAII STRAIN 7 GENE ST2
                    057)/CN
E11           1     UDP-N-ACETYLGLUCOSAMINE-DOLICHYL PYROPHOSPHATE N-ACETYLGLUCO
                    SAMINE N-ACETYLGLUCOSAMINYLTRANSFERASE/CN
E12           1     UDP-N-ACETYLGLUCOSAMINE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRA
                    NSFERASE/CN

=> s E4;D
L7            1 "UDP-N-ACETYLGLUCOSAMINE-2-EPIMERASE / N-ACETYLMANNOSAMINE KINAS
                E (HUMAN GENE UDP-GLCNAC-2-EPIMERASE)"/CN


L7   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2003 ACS on STN
RN   462370-10-1  REGISTRY
CN   GenBank CAB42607 (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   2909: PN: WO03038130 FIGURE: 3 claimed protein
CN   GenBank CAB42607 (Translated from: GenBank AJ238764)
CN   UDP-N-acetylglucosamine-2-epimerase / N-acetylmannosamine kinase
     (human gene UDP-GlcNAc-2-epimerase)
FS   PROTEIN SEQUENCE
MF   Unspecified
CI   MAN
SR   GenBank
LC   STN Files:   CA, CAPLUS

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
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